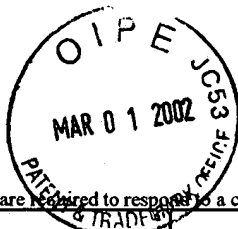


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				Filing Date	April 18, 2001
				First Named Inventor	MAYO, Stephen L.
				Group Art Unit	1636
Examiner Name	TECH CENTER 1600/2900				
Attorney Docket Number	A-65353-8/RFT/RMS/RMK				
Sheet	1	of	4		

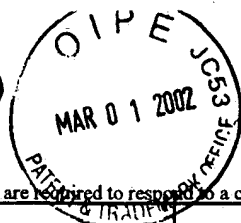
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sp	A1	Brenner and Berry, A., et al., "A quantitative methodology for the de novo design of proteins", Protein Sci. 3:1871-1882 (Oct. 1994).		
sp	A2	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) Oct. 6, 1997, 9-10 (1997).		
sp	A3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol.247:1306-1310 (Mar. 1990).		
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sp	A5	Brooks et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations," J. of Computational Chemistry, 4(2):187-217 (1983).		
sp	A6	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug. 1983).		
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sp	A8	Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", Protein Science 6:1333-1337 (Jun. 1997).		
sp	A9	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).		
sp	A10	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).		
sp	A11	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol. 4, Suppl. 2, 83 (1995).		
sp	A12	Dahiyat et al., "Protein design Automation," Poster Sessions, Protein Science vol.5, Suppl. 1, 22-23 (1996).		
sp	A13	Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 278:82-87 (1997).		
sp	A14	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).		
sp	A15	Dahiyat et al., "Protein Design Automation," 1996, Protein Science, vol. 5, pp. 895-903, Nov. 30, 1999.		
sp	A16	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).		
sp	A17	Dalal, S., et al., "Protein alchemy: Changing .beta.-sheet into .alpha.-helix", Nature Struc. Biol. vol.4(7):548-552 (Jul. 1997).		
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				First Named Inventor	MAYO, Stephen L.		
				Group Art Unit	1636		
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	B4	Desmet, J., et al., "The 'Dead End Elimination' Theorem: A New Approach to the Side Chain Packing Protein", from "The Protein Folding Problem and Tertiary Structure Prediction" Ch.10:1-49 (1994).	
	B5	Desmet, J., et al., "The dead-end elimination theorem and its use in protein side-chain positioning", Nature vol.356:539-542 (Apr. 1992).	
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	B7	Dunbrack Jr., R.L., et al., "Conformational analysis of the backbone-dependent rotamer preferences of protein sidechains", Struc. Biol. vol.1(5):334-340 (May 1994).	
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	B11	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils," Proc. Natl. Acad. Sci. USA, 92:8408-8412 (1995).	
	B12	Harbury et al., "High-Resolution Protein Design with Backbone Freedom," Science, 282:1462-1467 (1998).	
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	B14	Hellinga, H.W., "Rational protein design: Combining theory and experiment", Proc. Natl. Acad. Sci, USA vol.94:10015-10017 (Sep. 1997).	
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✓	C1	Jones, D.T., "De novo protein design using pairwise potentials and a genetic algorithm", Protein Science 3:567-574 (1994).	
	C2	Koehl et al., "De Novo Protein Design. I. In Search of Stability and Specificity," J. Mol. Biol., 293:1161-1181 (1999).	
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	C4	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded β -Sheet Protein," Science, 281:253-256 (1988).	
	C5	Lasters et al., "Enhanced dead-end elimination in the search for the global minimum energy conformation of a collection of protein side chains," 1995, Protein Engineering, vol. 8, No. 8, pp. 815-822.	
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	C7	Lazar et al., "De novo design of the hydrophobic core of ubiquitin," Protein Science 6:1167-1178 (1997).	
	C8	Lee et al., "Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core," Nature, 352:448-451 (1991).	
	C9	Lim et al., "The crystal structure of a mutant protein with altered but improved hydrophobic core packing," Proc Natl Acad Sci U S A. 1994 Jan 4;91(1):423-7	
	C10	Mayo et al., "DREIDING: A Generic Force Field for Molecular Simulations," J. Phys. Chem., 94:8897-8909 (1990).	
	C11	Minor Jr., D.L., "Measurement of the .beta.-sheet-forming propensities of amino acids", Nature vol.367:660-663 (Feb. 1994).	
	C12	Munoz, V., et al., "Helix design, prediction and stability", Curr. Opin. in Biotech. 6:382-386 (Aug. 1995).	
	C12	Munoz, V., et al., "Intrinsic Secondary Structure Propensities of the Amino Acids, Using Statistical phi-psi Matrices: Comparison with Experimental Scales", Proteins 20:301-311 (1994).	
	C14	Munoz, V., et al., "Analysis of the effect of local interactions on protein stability", Folding & Design 1(3):167-178 (Apr. 1996).	
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	C16	Padmanabhan, S., et al., "Relative helix-forming tendencies of nonpolar amino acids", Nature vol.344:268-270 (Mar. 1990).	
	C17	Ponder, J.W., et al., "Use of Packing Criteria in the Enumeration of Allowed Sequences for Different Structural Classes", release by Acad. Press Inc. (London) Ltd. pp.775-791(1987).	
	✓	C18	Rappe et al., "Charge Equilibration for Molecular Dynamics Simulations," J. Phys. Chem., 95:3358-3363 (1991).

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	D3	Stickle et al., "Hydrogen Bonding in Globular Proteins," (1992) Journal of Molecular Biology, vol.226, pp. 1143-1159.	
	D4	Sun, S., et al., "Designing amino acid sequences to fold with good hydrophobic cores", Protein Eng. vol.8(12):1205-1213 (1995).	
	D5	Tuffery et al., "A New Approach to the Rapid Determination of Protein Side Chain Conformations," J. of Biomolecular Struct. & Dynamics, 8(6):1267-1289 (1991).	
	D6	van Gunsteren et al., "Prediction of the Activity and Stability Effects of Site-directed Mutagenesis on a Protein Core," J. Mol. Biol., 227:389-395 (1992).	
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	D8	Wesson et al., "Atomic solvation parameters applied to molecular dynamics of proteins in solution," Protein Science, 1:227-235 (1992).	
	D9	Wodak, S.J., et al., "Analytical approximation to the accessible surface area of proteins", Proc. Natl. Acad. Sci. USA vol.77(4):1736-1740 (Apr. 1980).	

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